

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/516,795
Source: PCT
Date Processed by STIC: 12-17-09

ENTERED



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,795

DATE: 12/17/2004
TIME: 15:49:32

Input Set : N:\FATIMA\10516795.txt
Output Set: N:\CRF4\12172004\J516795.raw

3 <110> APPLICANT: Susan M. Freier
 4 Brenda F. Baker
 5 Kenneth W. Dobie
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING
 PROTEIN-1
 8 EXPRESSION
 10 <130> FILE REFERENCE: ISIS0046-500
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/516,795
 C--> 12 <141> CURRENT FILING DATE: 2004-12-03
 12 <150> PRIOR APPLICATION NUMBER: US 10/161996
 14 <151> PRIOR FILING DATE: 2002-06-04
 16 <160> NUMBER OF SEQ ID NOS: 273
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 20
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 26 <223> OTHER INFORMATION: Antisense Oligonucleotide
 28 <400> SEQUENCE: 1
 29 tccgtcatcg ctcctcaggg 20
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 20
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 39 <223> OTHER INFORMATION: Antisense Oligonucleotide
 41 <400> SEQUENCE: 2
 42 gtgcgcgcga gccgaaatc 20
 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 20
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 50 <220> FEATURE:
 52 <223> OTHER INFORMATION: Antisense Oligonucleotide
 54 <400> SEQUENCE: 3
 55 atgcattctg cccccaagga 20
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 4154
 60 <212> TYPE: DNA
 61 <213> ORGANISM: H. sapiens
 63 <220> FEATURE:
 65 <221> NAME/KEY: CDS
 66 <222> LOCATION: (167)...(3610)
 68 <400> SEQUENCE: 4

(PS, G)

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69	taacgaggaa	ctttcgccg	gcgcggggcc	gcctctgagg	ccagggcagg	acacgaacgc	60
71	gccccggc	ggcgccact	gagagccggg	gccgcggcgg	cgctccctag	gaagggccgt	120
73	acgaggcggc	gggcccggcg	ggcctcccg	aggaggcggc	tgcgcc	atg gac gag	175
74						Met Asp Glu	
75						1	
77	cca ccc ttc	agc gag gcg	gct ttg gag	cag gcg ctg	ggc gag ccg	tgc	223
78	Pro Pro Phe	Ser Glu Ala	Ala Leu Glu	Gln Ala	Leu Gly	Glu Pro Cys	
79	5		10		15		
81	gat ctg	gac gcg	ctg ctg	acc gac atc	gaa gac atg	ctt cag	271
82	Asp Leu Asp	Ala Ala Leu	Leu Thr Asp	Ile Glu Asp	Met Leu	Gln Leu	
83	20		25		30	35	
85	atc aac aac	caa gac agt	gac ttc	cct ggc	cta ttt gac	cca ccc tat	319
86	Ile Asn Asn	Gln Asp Ser	Asp Phe	Pro Gly	Leu Phe	Asp Pro Pro Tyr	
87			40		45	50	
89	gct ggg agt	ggg gca	ggg ggc	aca gac	cct gcc	agc ccc gat	367
90	Ala Gly Ser	Gly Ala	Gly Gly	Thr Asp Pro	Ala Ser Pro	Asp Thr Ser	
91		55		60		65	
93	tcc cca	ggc agc	ttg tct	cca cct	cct gcc	aca ttg agc	415
94	Ser Pro Gly	Ser Leu Ser	Pro Pro Ala	Thr Leu Ser	Ser Ser	Leu	
95		70		75		80	
97	gaa gcc	ttc ctg	agc ggg	ccg cag	gca gcg	ccc tca ccc	463
98	Glu Ala Phe	Leu Ser Gly	Pro Gln Ala	Ala Pro Ser	Pro Leu Ser	Pro	
99		85		90		95	
101	ccc cag	cct gca	ccc act	cca ttg	aag atg	tac ccg tcc atg	511
102	Pro Gln Pro	Ala Pro Thr	Pro Leu Lys	Met Tyr	Pro Ser	Met Pro Ala	
103	100		105		110		115
105	ttc tcc	cct ggg	cct ggt	atc aag	gaa gag	tca gtg cca	559
106	Phe Ser Pro	Gly Pro Gly	Ile Lys Glu	Glu Ser Val	Pro Leu	Ser Ile	
107			120		125		130
109	ctg cag acc	ccc acc cca	cag ccc	ctg cca	ggg gcc	ctc ctg cca	607
110	Leu Gln Thr	Pro Thr Pro	Gln Pro Leu	Pro Gly Ala	Leu Leu	Pro Gln	
111		135		140		145	
113	agc ttc cca	gcc cca	gcc cca	cog cag	ttc agc	tcc acc cct gtg	655
114	Ser Phe Pro	Ala Pro Pro	Gln Phe Ser	Ser Thr Pro	Val Leu		
115		150		155		160	
117	ggc tac ccc	agc cct	ccg gga	ggc ttc	tct aca	gga agc	703
118	Gly Tyr Pro	Ser Pro Pro	Gly Gly	Phe Ser Thr	Gly Ser Pro	Pro Gly	
119		165		170		175	
121	aac acc cag	cag ccg	ctg cct	ggc ctg	cca ctg	gct tcc ccg	751
122	Asn Thr Gln	Gln Pro Leu	Pro Gly Leu	Pro Leu Ala	Ser Pro	Pro Pro Gly	
123		180		185		190	195
125	gtc ccg	ccc gtc	tcc ttg	cac acc	cag gtc	cag agt gtg	799
126	Val Pro Pro	Val Ser Leu	His Thr Gln	Val Gln	Ser Val	Val Pro Gln	
127		200		205		210	
129	cag cta	ctg aca	gtc aca	gct gcc	ccc acg	gca gcc	847
130	Gln Leu Leu	Thr Val Thr	Ala Ala Pro	Thr Ala	Ala Pro	Val Thr Thr	
131		215		220		225	
133	act gtg acc	tcg cag	atc cag	cag gtc	ccg gtc	ctg ctg cag	895
134	Thr Val Thr	Ser Gln Ile	Gln Val Pro	Val Leu	Leu Gln	Pro His	

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135	230	235	240	
137	ttc atc aag gca gac tcg ctg ctt ctg aca gcc atg aag aca gac gga			943
138	Phe Ile Lys Ala Asp Ser Leu Leu Leu Thr Ala Met Lys Thr Asp Gly			
139	245	250	255	
141	gcc act gtg aag gcg gca ggt ctc agt ccc ctg gtc tct ggc acc act			991
142	Ala Thr Val Lys Ala Ala Gly Leu Ser Pro Leu Val Ser Gly Thr Thr			
143	260	265	270	275
145	gtg cag aca ggg cct ttg ccg acc ctg gtg agt ggc gga acc atc ttg			1039
146	Val Gln Thr Gly Pro Leu Pro Thr Leu Val Ser Gly Gly Thr Ile Leu			
147	280	285	290	
149	gca aca gtc cca ctg gtc gta gat gcg gag aag ctg cct atc aac cg			1087
150	Ala Thr Val Pro Leu Val Val Asp Ala Glu Lys Leu Pro Ile Asn Arg			
151	295	300	305	
153	ctc gca gct ggc agc aag gcc ccg gcc tct gcc cag agc cgt gga gag			1135
154	Leu Ala Ala Gly Ser Lys Ala Pro Ala Ser Ala Gln Ser Arg Gly Glu			
155	310	315	320	
157	aag cgc aca gcc cac aac gcc att gag aag cgc tac cgc tcc tcc atc			1183
158	Lys Arg Thr Ala His Asn Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile			
159	325	330	335	
161	aat gac aaa atc att gag ctc aag gat ctg gtg gtc act gag gca			1231
162	Asn Asp Lys Ile Ile Glu Leu Lys Asp Leu Val Val Gly Thr Glu Ala			
163	340	345	350	355
165	aag ctg aat aaa tct gct gtc ttg cgc aag gcc atc gac tac att cgc			1279
166	Lys Leu Asn Lys Ser Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg			
167	360	365	370	
169	ttt ctg caa cac agc aac cag aaa ctc aag cag gag aac cta agt ctg			1327
170	Phe Leu Gln His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu			
171	375	380	385	
173	cgc act gtc cac aaa agc aaa tct ctg aag gat ctg gtg tcg gcc			1375
174	Arg Thr Ala Val His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala			
175	390	395	400	
177	tgt ggc agt gga ggg aac aca gac gtg ctc atg gag ggc gtg aag act			1423
178	Cys Gly Ser Gly Gly Asn Thr Asp Val Leu Met Glu Gly Val Lys Thr			
179	405	410	415	
181	gag gtg gag gac aca ctg acc cca ccc ccc tcg gat gct ggc tca cct			1471
182	Glu Val Glu Asp Thr Leu Thr Pro Pro Ser Asp Ala Gly Ser Pro			
183	420	425	430	435
185	ttc cag agc agc ccc ttg tcc ctt ggc agc agg ggc agt ggc agc ggt			1519
186	Phe Gln Ser Ser Pro Leu Ser Leu Gly Ser Arg Gly Ser Gly Ser Gly			
187	440	445	450	
189	ggc agt ggc agt gac tcg gag cct gac agc cca gtc ttt gag gac agc			1567
190	Gly Ser Gly Ser Asp Ser Glu Pro Asp Ser Pro Val Phe Glu Asp Ser			
191	455	460	465	
193	aag gca aag cca gag cag cgg ccg tct ctg cac agc cgg ggc atg ctg			1615
194	Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg Gly Met Leu			
195	470	475	480	
197	gac cgc tcc cgc ctg gcc ctg tgc acg ctc gtc ttc ctc tgc ctg tcc			1663
198	Asp Arg Ser Arg Leu Ala Leu Cys Thr Leu Val Phe Leu Cys Leu Ser			
199	485	490	495	

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201	tgc aac ccc ttg gcc tcc ttg ctg ggg gcc cgg ggg ctt ccc agc ccc	1711
202	Cys Asn Pro Leu Ala Ser Leu Leu Gly Ala Arg Gly Leu Pro Ser Pro	
203	500 505 510 515	
205	tca gat acc acc agc gtc tac cat agc cct ggg cgc aac gtg ctg ggc	1759
206	Ser Asp Thr Thr Ser Val Tyr His Ser Pro Gly Arg Asn Val Leu Gly	
207	520 525 530	
209	acc gag agc aga gat ggc cct ggc tgg gcc cag tgg ctg ctg ccc cca	1807
210	Thr Glu Ser Arg Asp Gly Pro Gly Trp Ala Gln Trp Leu Leu Pro Pro	
211	535 540 545	
213	gtg gtc tgg ctg ctc aat ggg ctg tgg gtg ctc gtc tcc ttg gtg ctt	1855
214	Val Val Trp Leu Leu Asn Gly Leu Leu Val Leu Val Ser Leu Val Leu	
215	550 555 560	
217	ctc ttt gtc tac ggt gag cca gtc aca cgg ccc cac tca ggc ccc gcc	1903
218	Leu Phe Val Tyr Gly Glu Pro Val Thr Arg Pro His Ser Gly Pro Ala	
219	565 570 575	
221	gtg tac ttc tgg agg cat cgc aag cag gct gac ctg gac ctg gcc cgg	1951
222	Val Tyr Phe Trp Arg His Arg Lys Gln Ala Asp Leu Asp Leu Ala Arg	
223	580 585 590 595	
225	gga gac ttt gcc cag gct gcc cag cag ctg tgg ctg gcc ctg cgg gca	1999
226	Gly Asp Phe Ala Gln Ala Ala Gln Gln Leu Trp Leu Ala Leu Arg Ala	
227	600 605 610	
229	ctg ggc cgg ccc ctg ccc acc tcc cac ctg gac ctg gct tgt agc ctc	2047
230	Leu Gly Arg Pro Leu Pro Thr Ser His Leu Asp Leu Ala Cys Ser Leu	
231	615 620 625	
233	ctc tgg aac ctc atc cgt cac ctg ctg cag cgt ctc tgg gtg ggc cgc	2095
234	Leu Trp Asn Leu Ile Arg His Leu Leu Gln Arg Leu Trp Val Gly Arg	
235	630 635 640	
237	tgg ctg gca ggc cgg gca ggg ggc ctg cag cag gac tgt gct ctg cga	2143
238	Trp Leu Ala Gly Arg Ala Gly Gly Leu Gln Gln Asp Cys Ala Leu Arg	
239	645 650 655	
241	gtg gat gct agc gcc agc gcc cga gac gca gcc ctg gtc tac cat aag	2191
242	Val Asp Ala Ser Ala Ser Ala Arg Asp Ala Ala Leu Val Tyr His Lys	
243	660 665 670 675	
245	ctg cac cag ctg cac acc atg ggg aag cac aca ggc ggg cac ctc act	2239
246	Leu His Gln Leu His Thr Met Gly Lys His Thr Gly Gly His Leu Thr	
247	680 685 690	
249	gcc acc aac ctg gcg ctg agt gcc ctg aac ctg gca gag tgt gca ggg	2287
250	Ala Thr Asn Leu Ala Leu Ser Ala Leu Asn Leu Ala Glu Cys Ala Gly	
251	695 700 705	
253	gat gcc gtg tct gtg gcg acg ctg gcc gag atc tat gtg gcg gct gca	2335
254	Asp Ala Val Ser Val Ala Thr Leu Ala Glu Ile Tyr Val Ala Ala Ala	
255	710 715 720	
257	ttg aga gtg aag acc agt ctc cca cgg gcc ttg cat ttt ctg aca cgc	2383
258	Leu Arg Val Lys Thr Ser Leu Pro Arg Ala Leu His Phe Leu Thr Arg	
259	725 730 735	
261	ttc ttc ctg agc agt gcc cgc cag gcc tgc ctg gca cag agt ggc tca	2431
262	Phe Phe Leu Ser Ser Ala Arg Gln Ala Cys Leu Ala Gln Ser Gly Ser	
263	740 745 750 755	
265	gtg cct cct gcc atg cag tgg ctc tgc cac ccc gtg ggc cac cgt ttc	2479

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266 Val Pro Pro Ala Met Gln Trp Leu Cys His Pro Val Gly His Arg Phe			
267 760	765	770	
269 ttc gtg gat ggg gac tgg tcc gtg ctc agt acc cca tgg gag agc ctg			2527
270 Phe Val Asp Gly Asp Trp Ser Val Leu Ser Thr Pro Trp Glu Ser Leu			
271 775	780	785	
273 tac agc ttg gcc ggg aac cca gtg gac ccc ctg gcc cag gtg act cag			2575
274 Tyr Ser Leu Ala Gly Asn Pro Val Asp Pro Leu Ala Gln Val Thr Gln			
275 790	795	800	
277 cta ttc cgg gaa cat ctc tta gag cga gca ctg aac tgt gtg acc cag			2623
278 Leu Phe Arg Glu His Leu Leu Glu Arg Ala Leu Asn Cys Val Thr Gln			
279 805	810	815	
281 ccc aac ccc agc cct ggg tca gct gat ggg gac aag gaa ttc tcg gat			2671
282 Pro Asn Pro Ser Pro Gly Ser Ala Asp Gly Asp Lys Glu Phe Ser Asp			
283 820	825	830	835
285 gcc ctc ggg tac ctg cag ctg aac agc tgt tct gat gct gcg ggg			2719
286 Ala Leu Gly Tyr Leu Gln Leu Leu Asn Ser Cys Ser Asp Ala Ala Gly			
287 840	845	850	
289 gct cct gcc tac agc ttc tcc atc agt tcc agc atg gcc acc acc acc			2767
290 Ala Pro Ala Tyr Ser Phe Ser Ile Ser Ser Met Ala Thr Thr Thr			
291 855	860	865	
293 ggc gta gac ccg gtg gcc aag tgg tgg gcc tct ctg aca gct gtg gtg			2815
294 Gly Val Asp Pro Val Ala Lys Trp Trp Ala Ser Leu Thr Ala Val Val			
295 870	875	880	
297 atc cac tgg ctg ccg cgg gat gag gag gcg gct gag cgg ctg tgc ccg			2863
298 Ile His Trp Leu Arg Arg Asp Glu Glu Ala Ala Glu Arg Leu Cys Pro			
299 885	890	895	
301 ctg gtg gag cac ctg ccc ccg gtg ctg cag gag tct gag aga ccc ctg			2911
302 Leu Val Glu His Leu Pro Arg Val Leu Gln Glu Ser Glu Arg Pro Leu			
303 900	905	910	915
305 ccc agg gca gct ctg cac tcc ttc aag gct gcc ccg gcc ctg ctg ggc			2959
306 Pro Arg Ala Ala Leu His Ser Phe Lys Ala Ala Arg Ala Leu Leu Gly			
307 920	925	930	
309 tgt gcc aag gca gag tct ggt cca gcc agc ctg acc atc tgt gag aag			3007
310 Cys Ala Lys Ala Glu Ser Gly Pro Ala Ser Leu Thr Ile Cys Glu Lys			
311 935	940	945	
313 gcc agt ggg tac ctg cag gac agc ctg gct acc aca cca gcc agc agc			3055
314 Ala Ser Gly Tyr Leu Gln Asp Ser Leu Ala Thr Thr Pro Ala Ser Ser			
315 950	955	960	
317 tcc att gac aag gcc gtg cag ctg ttc ctg tgt gac ctg ctt ctt gtg			3103
318 Ser Ile Asp Lys Ala Val Gln Leu Phe Leu Cys Asp Leu Leu Val			
319 965	970	975	
321 gtg cgc acc agc ctg tgg ccg cag cag cag ccc ccg gcc ccg cca			3151
322 Val Arg Thr Ser Leu Trp Arg Gln Gln Gln Pro Pro Ala Pro Ala Pro			
323 980	985	990	995
325 gca gcc cag ggc gcc agc agc agg ccc cag gct tcc gcc ctt gag ctg			3199
326 Ala Ala Gln Gly Ala Ser Ser Arg Pro Gln Ala Ser Ala Leu Glu Leu			
327 1000	1005	1010	
329 cgt ggc ttc caa ccg gac ctg agc agc ctg agg ccg ctg gca cag agc			3247
330 Arg Gly Phe Gln Arg Asp Leu Ser Ser Leu Arg Arg Leu Ala Gln Ser			

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:99; N Pos. 352,415
Seq#:100; N Pos. 3861,3862,3863,3864,3865,3866,3867,3868,3869,3870,3871
Seq#:100; N Pos. 3872,3873,3874,3875,3876,3877,3878,3879,3880,3881,3882
Seq#:100; N Pos. 3883,3884,3885,3886,3887,3888,3889,3890,3891,3892,3893
Seq#:100; N Pos. 3894,3895,3896,3897,3898,3899,3900,3901,3902,3903,3904
Seq#:100; N Pos. 3905,3906,3907,3908,3909,3910,3911,3912,3913,3914,3915
Seq#:100; N Pos. 3916,3917,3918,3919,3920,3921,3922,3923,3924,3925,3926
Seq#:100; N Pos. 3927,3928,3929,3930,3931,3932,3933,3934,3935,3936,3937
Seq#:100; N Pos. 3938,3939,3940,3941,3942,3943,3944,3945,3946,3947,3948
Seq#:100; N Pos. 3949,3950,3951,3952,3953,3954,3955,3956,3957,3958,3959
Seq#:100; N Pos. 3960

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3001 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:99,Line#:2997
L:3012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:300
M:341 Repeated in SeqNo=99
L:3161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:3840
M:341 Repeated in SeqNo=100